SEQUENCE LISTING <110> SIREEN AG <120> Methods of identifying, selecting and/or characterizing compounds which modulate the activity of a Src familiy kinase <130> SI07P001W0 <150> EP 03028713.0 <151> 2003-12-12 <160> 51 <170> PatentIn version 3.1 <210> 1 <211> 536 <212> PRT <213> Homo sapiens <220> <221> MISC_FEATURE <223> Description of sequence: Src-KA <400> 1 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg 5 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe 50 55

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 140

Ser Il 145	e Gln	Ala	Glu	Glu 150	Trp	Tyr	Phe	Gly	Lys 155	Ile	Thr	Arg	Arg	Glu 160
Ser Gl	u Arg	Leu	Leu 165	Leu	Asn	Ala	Glu	Asn 170	Pro	Arg	Gly	Thr	Phe 175	Leu
Val Ar	g Glu	Ser 180	Glu	Thr	Thr	Lys	Gly 185	Ala	Tyr	Cys	Leu	Ser 190	Val	Ser
Asp Ph	e Asp 195	Asn	Ala	Lys	Gly	Leu 200	Asn	Val	Lys	His	Tyr 205	Lys	Ile	Arg
Lys Le 21		Ser	Gly	Gly	Phe 215	Tyr	Ile	Thr	Ser	Arg 220	Thr	Gln	Phe	Asn
Ser Le 225	u Gln	Gln	Leu	Val 230	Ala	Tyr	Tyr	Ser	Lys 235	His	Ala	Asp	Gly	Leu 240.
Cys Hi	s Arg	Leu	Thr 245	Thr	Val	Cys	Pro	Thr 250	Ser	Lys	Pro	Gln	Thr 255	Gln
Gly Le	u Ala	Lys 260	Asp	Ala	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Arg	Leu
Glu Va	l Lys 275	Leu	Gly	Gln	Gly	Cys 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp As 29	0				295					300				
305	r Pro			310					315					320
Arg Hi			325					330					335	
Ile Ty:		340					345					350		
Leu Lys	355					360					365			
Met Ala)				375					380				
Tyr Val 385	. His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Glu	Asn 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val 450 450 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg 465 470 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu 530 535

<210> 2

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Src-TQ

<400> 2

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg 1 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe

55 60 50 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 85 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 135 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 150 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 185 180 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 195 200 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 215 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu 230 235 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln 245 250 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr 290 295 300

Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Gln	Glu	Ala	Gln 315	Val	Met	Lys	Lys	Leu 320
Arg	His	Glu	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Gln	Glu	Tyr	Met	Ser 345	Lys	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Gly 355	Glu	Thr	Gly	Lys	Tyr 360	Leu	Arg	Leu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ser 375	Gly	Met	Ala	Tyr	Val 380	Glu	Arg	Met	Asn
Tyr 385	Val	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Glu	Asn 400
Leu	Val	Cys	Lys	Val 405	Ala	Asp	Phe	Gly	Leu 410	Ala	Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Tyr	Gly 440	Arg	Phe	Thr	Ile	Lys 445	Ser	Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455	Thr	Glu	Leu	Thr	Thr 460	Lys	Gly	Arg	Val
Pro 465	Tyr	Pro	Gly	Met	Val 470	Asn	Arg	Glu	Val	Leu 475	Asp	Gln	Val	Glu	Arg 480
Gly	Tyr	Arg	Met	Pro 485	Cys	Pro	Pro	Glu	Cys 490	Pro	Glu	Ser	Leu	His 495	Asp
Leu	Met	Cys	Gln 500	Cys	Trp	Arg	Lys	Glu 505	Pro	Glu	Glu	Arg	Pro 510	Thr	Phe
Glu	Tyr	Leu 515	Gln	Ala	Phe	Leu	Glu 520	Asp	Tyr	Phe	Thr	Ser 525	Thr	Glu	Pro
Gln	Tyr 530	Gln	Pro	Gly	Glu	Asn 535	Leu								

<210> 3 <211> 536 <212> PRT

											6/10)3			
<21	3>]	Homo	sap:	iens											
<22: <22: <22:	1> 1		_feat		of se	eque	nce:	Src	-YF						
<40	0>	3						•							
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Ser	Leu	Glu	Pro 20	Ala	Glu	Asn	Val	His 25	Gly	Ala	Gly	Gly	Gly 30	Ala	Phe
Pro	Ala	Ser 35	Gln	Thr	Pro	Ser	Lys 40	Pro	Ala	Ser	Ala	Asp 45	Gly	His	Arg
Gly	Pro 50	Ser	Ala	Ala	Phe	Ala 55	Pro	Ala	Ala	Ala	Glu 60	Pro	Lys	Leu	Phe
Gly 65	Gly	Phe	Asn	Ser	Ser 70	Asp	Thr	Val	Thr	Ser 75	Pro	Gln	Arg	Ala	Gly 80
Pro	Leu	Ala	Gly	Gly 85	Val	Thr	Thr	Phe	Val 90	Ala	Leu	Tyr	Asp	Tyr 95	Glu
Ser	Arg	Thr	Glu 100	Thr	Asp	Leu	Ser	Phe 105	Lys	Lys	Gly	Glu	Arg 110	Leu	Gln
Ile	Val	Asn 115	Asn	Thr	Glu	Gly	Asp 120	Trp	Trp	Leu	Ala	His 125	Ser	Leu	Ser
Thr	Gly 130	Gln	Thr	Gly	Tyr	Ile 135	Pro	Ser	Asn	Tyr	Val 140	Ala	Pro	Ser	Asp
Ser 145	Ile	Gln	Ala	Glu	Glu 150	Trp	Tyr	Phe	Gly	Lys 155	Ile	Thr	Arg	Arg	Glu 160
Ser	Glu	Arg	Leu	Leu 165	Leu	Asn	Ala	Glu	Asn 170	Pro	Arg	Gly	Thr	Phe 175	Leu
Val	Arg	Glu	Ser 180	Glu	Thr	Thr	Lys	Gly 185	Ala	Tyr	Cys	Leu	Ser 190	Val	Ser
Asp	Phe	Asp 195	Asn	Ala	Lys	Gly	Leu 200	Asn	Val	Lys	His	Tyr 205	Lys	Ile	Arg

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 210 215 220

Ser 225	Leu	Gln	Gln	Leu	Val 230	Ala	Tyr	Tyr	Ser	Lys 235	His	Ala	Asp	Gly	Leu 240
Cys	His	Arg	Leu	Thr 245	Thr	Val	Суз	Pro	Thr 250	Ser	Lys	Pro	Gln	Thr 255	Gln
Gly	Leu	Ala	Lys 260	Asp	Ala	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Arg	Leu
Glu	Val	Lys 275	Leu	Gly	Gln	Gly	Cys 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Arg	Val 295	Ala	Ile	Lys	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Gln	Glu	Ala	Gln 315	Val	Met	Lys	Lys	Leu 320
Arg	His	Glu	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Tyr	Met	Ser 345	Lys	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Gly 355	Glu	Thr	Gly	Lys	Tyr 360	Leu	Arg	Leu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ser 375	Gly	Met	Ala	Tyr	Val 380	Glu	Arg	Met	Asn
Tyr 385	Val	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Glu	Asn 400
Leu	Val	Cys	Lys	Val 405	Ala	Asp	Phe	Gly	Leu 410	Ala	Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Tyr	Gly 440	Arg	Phe	Thr	Ile	Lys 445	Ser	Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455	Thr	Glu	Leu	Thr	Thr 460	Lys	Gly	Arg	Val

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg

480 465 470 475

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Glu Asn Leu

<210> 4

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Src-TQ/YF

<400> 4

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg 40

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Glu Pro Lys Leu Phe

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly 70

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 8.5 90

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 100 105

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 115 120 125

Thr	Gly	Gln	Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Ser	Asp	
	130					135					140					

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 150

Ser Glu Arg Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 185

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 200

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 215

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu 230

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln 245

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu 265 260

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr 275 280

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr 290 295

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 315 320 305 310

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335

Ile Tyr Ile Val Gln Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe 340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn 370 375

10/103

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn 390 395

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 · 410

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 505

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515 520

Gln Phe Gln Pro Gly Glu Asn Leu 530

<210> 5

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> Description of sequence: Yes-KA

<400> . 5

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 25 20

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 35 40 45

Gly	Thr 50	Ala	Val	Asn	Phe	Ser 55	Ser	Leu	Ser	Met	Thr 60	Pro	Phe	Gly	Gly
Ser 65	Ser	Gly	Val	Thr	Pro 70	Phe	Gly	Gly	Ala	Ser 75	Ser	Ser	Phe	Ser	Val 80
Val	Pro	Ser	Ser	Tyr 85	Pro	Ala	Gly	Leu	Thr 90	Gly	Gly	Val	Thr	Ile 95	Phe
Val	Ala	Leu	Tyr 100	Asp	Tyr	Glu	Ala	Arg 105	Thr	Thr	Glu	Asp	Leu 110	Ser	Phe
Lys	Lys	Gly 115	Glu	Arg	Phe	Gln	Ile 120	Ile	Asn	Asn	Thr	Glu 125	Gly	Asp	Trp
Trp	Glu 130	Ala	Arg	Ser	Ile	Ala 135	Thr	Gly	Lys	Asn	Gly 140	Tyr	Ile	Pro	Ser
Asn 145	Tyr	Val	Ala	Pro	Ala 150	Asp	Ser	Ile	Gln	Ala 155	Glu	Glu	Trp	Tyr	Phe 160
Gly	Lys	Met	Gly	Arg 165	Lys	Asp	Ala	Glu	Arg 170	Leu	Leu	Leu	Asn	Pro 175	Gly
Asn	Gln	Arg	Gly 180	Ile	Phe	Leu	Val	Arg 185	Glu	Ser	Glu	Thr	Thr 190	Lys	Gly
Ala	Tyr	Ser 195	Leu	Ser	Ile	Arg	Asp 200	Trp	Asp	Glu	Ile	Arg 205	Gly	Asp	Asn
Val	Lys 210	His	Tyr	Lys	Ile	Arg 215	Lys	Leu	Asp	Asn	Gly 220	Gly	Tyr	Tyr	Ile
Thr 225	Thr	Arg	Ala	Gln	Phe 230	Asp	Thr	Leu	Gln	Lys 235	Leu	Val	Lys	His	Tyr 240
Thr	Glu	His	Ala	Asp 245	Gly	Leu	Cys	His	Lys 250	Leu	Thr	Thr	Val	Cys 255	Pro
Thr	Val	Lуs	Pro 260	Gln	Thr	Gln	Gly	Leu 265	Ala	Lys	Asp	Ala	Trp 270	Glu	Ile
Pro	Arg	Glu 275	Ser	Leu	Arg	Leu	Glu 280	Val	Lys	Leu	Gly	Gln 285	Gly	Cys	Phe

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile

-	2	1-	α	3
				•

295 300 290 Ala Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 310 315 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr 330 325 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser 345 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu 360 365 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 375 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 395 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly 410 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 420 425 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu 455 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 470 475 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly 485 490 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 520 525 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu 540 530 535

<210> 6 <211> 543 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Description of sequence: Yes-TQ <400> 6 Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr 10 Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 25 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 100 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp 120 115 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 130 135 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 145 150 155 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Asn Pro Gly 170 175 165

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly 180

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn 200 205 195

Val	Lys 210	His	Tyr	Lys	Ile	Arg 215	Lys	Leu	Asp	Asn	Gly 220	Gly	Tyr	Tyr	Ile
Thr 225	Thr	Arg	Ala	Gln	Phe 230	Asp	Thr	Leu	Gln	Lys 235	Leu	Val	Lys	His	Tyr 240
Thr	Glu	His	Ala	Asp 245	Gly	Leu	Cys	His	Lys 250	Leu	Thr	Thr	Val	Cys 255	Pro
Thr	Val	Lys	Pro 260	Gln	Thr	Gln	Gly	Leu 265	Ala	Lys	Asp	Ala	Trp 270	Glu	Ile
Pro	Arg	Glu 275	Ser	Leu	Arg	Leu	Glu 280	Val	Lys	Leu	Gly	Gln 285	Gly	Суз	Phe
Gly	Glu 290	Val	Trp	Met	Gly	Thr 295	Trp	Asn	Gly	Thr	Thr 300	Lys	Val	Ala	Ile
Lys 305	Thr	Leu	Lys	Pro	Gly 310	Thr	Met	Met	Pro	Glu 315	Ala	Phe	Leu	Gln	Glu 320
Ala	Gln	Ile	Met	Lys 325	Lys	Leu	Arg	His	Asp 330	Lys	Leu	Val	Pro	Leu 335	Tyr
Ala	Val	Val	Ser 340	Glu	Glu	Pro	Ile	Tyr 345	Ile	Val	Gln	Glu	Phe 350	Met	Ser
Lys	Gly	Ser 355	Leu	Leu	Asp	Phe	Leu 360	Lys	Glu	Gly	Asp	Gly 365	Lys	Tyr	Leu
Lys	Leu 370	Pro	Gln	Leu	Val	Asp 375	Met	Ala	Ala	Gln	Ile 380	Ala	Asp	Gly	Met
Ala 385	Tyr	Ile	Glu	Arg	Met 390	Asn	Tyr	Ile	His	Arg 395	Asp	Leu	Arg	Ala	Ala 400
Asn	Ile	Leu	Val	Gly 405	Glu	Asn	Leu	Val	Cys 410	Lys	Ile	Ala	Asp	Phe 415	Gly
Leu	Ala	Arg	Leu 420	Ile	Glu	Asp	Asn	Glu 425	Tyr	Thr	Ala	Arg	G1n 430	Gly	Ala
Lys	Phe	Pro 435	Ile	Lys	Trp	Thr	Ala 440	Pro	Glu	Ala	Ala	Leu 445	Tyr	Gly	Arg

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
485 490 · 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 535 540

<210> 7

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Yes-YF

<400> 7

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp

115	120	125

115		120	125	
Trp Glu Ala Ar 130	rg Ser Ile Ala 135	Thr Gly Lys	Asn Gly Tyr 140	Ile Pro Ser
Asn Tyr Val Al 145	a Pro Ala Asp 150	Ser Ile Gln	Ala Glu Glu 155	Trp Tyr Phe 160
Gly Lys Met Gl	Ly Arg Lys Asp 165	Ala Glu Arg 170	Leu Leu Leu	Asn Pro Gly 175
Asn Gln Arg Gl 18	Ly Ile Phe Leu 30	Val Arg Glu 185	Ser Glu Thr	Thr Lys Gly 190
Ala Tyr Ser Le 195	eu Ser Ile Arg	Asp Trp Asp 200	Glu Ile Arg 205	Gly Asp Asn
Val Lys His Ty 210	yr Lys Ile Arg 215	Lys Leu Asp	Asn Gly Gly 220	Tyr Tyr Ile
Thr Thr Arg Al 225	la Gln Phe Asp 230	Thr Leu Gln	Lys Leu Val 235	Lys His Tyr 240
Thr Glu His Al	la Asp Gly Leu 245	Cys His Lys 250	Leu Thr Thr	Val Cys Pro 255
Thr Val Lys Pr 26	co Gln Thr Gln 50	Gly Leu Ala 265	Lys Asp Ala	Trp Glu Ile 270
Pro Arg Glu Se 275	er Leu Arg Leu	Glu Val Lys 280	Leu Gly Gln 285	Gly Cys Phe
Gly Glu Val Tr 290	rp Met Gly Thr 295	Trp Asn Gly	Thr Thr Lys 300	Val Ala Ile
Lys Thr Leu Ly 305	ys Pro Gly Thr 310	Met Met Pro	Glu Ala Phe 315	Leu Gln Glu 320
Ala Gln Ile Me	et Lys Lys Leu 325	Arg His Asp 330	Lys Leu Val	Pro Leu Tyr 335
Ala Val Val Se		Ile Tyr Ile 345	Val Thr Glu	Phe Met Ser 350
Lys Gly Ser Le 355	eu Leu Asp Phe	Leu Lys Glu 360	Gly Asp Gly 365	Lys Tyr Leu

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Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 375

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 425

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg 440

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly 490

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 505

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520

Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu 530 535

<210> 8

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> Description of sequence: Yes-TQ/YF

<400> 8

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 25 30

Gly	Ala	Glu 35	Pro	Thr	Thr	Val	Ser 40	Pro	Cys	Pro	Ser	Ser 45	Ser	Ala	Lys
Gly	Thr 50	Ala	Val	Asn	Phe	Ser 55	Ser	Leu	Ser	Met	Thr 60	Pro	Phe	Gly	Gly
Ser 65	Ser	Gly	Val	Thr	Pro 70	Phe	Gly	Gly	Ala	Ser 75	Ser	Ser	Phe	Ser	Val 80
Val	Pro	Ser	Ser	Tyr 85	Pro	Ala	Gly	Leu	Thr 90	Gly	Gly	Val	Thr	Ile 95	Phe
Val	Ala	Leu	Tyr 100	Asp	Tyr	Glu	Ala	Arg 105	Thr	Thr	Glu	Asp	Leu 110	Ser	Phe
Lys	Lys	Gly 115	Glu	Arg	Phe	Gln	Ile 120	Ile	Asn	Asn	Thr	Glu 125	Gly	Asp	Trp
Trp	Glu 130	Ala	Arg	Ser	Ile	Ala 135	Thr	Gly	Lys	Asn	Gly 140	Tyr	Ile	Pro	Ser
Asn 145	Tyr	Val	Ala	Pro	Ala 150	Asp	Ser	Ile	Gln	Ala 155	Glu	Glu	Trp	Tyr	Phe 160
Gly	Lys	Met	Gly	Arg 165	Lys	Asp	Ala	Glu	Arg 170	Leu	Leu	Leu	Asn	Pro 175	Gly
Asn	Gln	Arg	Gly 180	Ile	Phe	Leu	Val	Arg 185	Glu	Ser	Glu	Thr	Thr 190	Lys	Gly
Ala	Tyr	Ser 195	Leu	Ser	Ile	Arg	Asp 200	Trp	Asp	Glu	Ile	Arg 205	Gly	Asp	Asn
Val	Lys 210	His	Tyr	Lys	Ile	Arg 215	Lys	Leu	Asp	Asn	Gly 220	Gly	Tyr	Tyr	Ile
Thr 225	Thr	Arg	Ala	Gln	Phe 230	Asp	Thr	Leu	Gln	Lys 235	Leu	Val	Lys	His	Tyr 240
Thr	Glu	His	Ala	Asp 245	Gly	Leu	Cys	His	Lys 250	Leu	Thr	Thr	Val	Cys 255	Pro
Thr	Val	Lys	Pro 260	Gln	Thr	Gln	Gly	Leu 265	Ala	Lys	Asp	Ala	Trp 270	Glu	Ile
Pro	Arg	Glu 275	Ser	Leu	Arg	Leu	Glu 280	Val	Lys	Leu	Gly	Gln 285	Gly	Cys	Phe

275 280

Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile
	290					295					300				

- Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 305 310 315 320
- Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr 325 330 335
- Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser 340 345 350
- Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu 355 360 365
- Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 370 375 380
- Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 385 390 395
- Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly 405 410 415
- Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 420 425 430
- Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg 435 440 445
- Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu 450 460
- Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 465 470 475 480
- Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
- Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 510
- Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520 525
- Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu

20/103 530 535 540 <210> 9 <211> 529 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Description of sequence: Fgr-KA <400> 9 Met Gly Cys Val Phe Cys Lys Leu Glu Pro Val Ala Thr Ala Lys Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 120

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 135

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 155

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr 170

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly 185 180

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Asp	His	Val 195	Lys	His	Tyr	Lys	Ile 200	Arg	Lys	Leu	Asp	Met 205	Gly	Gly	Tyr
Tyr	Ile 210	Thr	Thr	Arg	Val	Gln 215	Phe	Asn	Ser	Val	Gln 220	Glu	Leu	Val	Gln

- His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro 225 230 235 240
- Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp 245 250 255
- Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly 260 265 270
- Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val 275 280 285
- Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu 290 295 300
- Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 305 310 315 320
- Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe 325 330 335
- Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 340 345 350
- Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu 355 360 365
- Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 370 375 380
- Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 385 390 395 400
- Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln \$405\$
- Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 420 425 430
- Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445

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Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 515 520 525

Thr

<210> 10

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fgr-TQ

<400> 10

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp $20 \hspace{1cm} 25 \hspace{1cm} 30$

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105 110

Asp	Trp	Trp 115	Glu	Ala	Arg	Ser	Leu 120	Ser	Ser	Gly	Lys	Thr 125	Gly	Cys	Ile
Pro	Ser 130	Asn	Tyr	Val	Ala	Pro 135	Val	Asp	Ser	Ile	Gln 140	Ala	Glu	Glu	Trp
Tyr 145	Phe	Gly	Lys	Ile	Gly 150	Arg	Lys	Asp	Ala	Glu 155	Arg	Gln	Leu	Leu	Ser 160
Pro	Gly	Asn	Pro	Gln 165	Gly	Ala	Phe	Leu	Ile 170	Arg	Glu	Ser	Glu	Thr 175	Thr
Lys	Gly	Ala	Tyr 180	Ser	Leu	Ser	Ile	Arg 185	Asp	Trp	Asp	Gln	Thr 190	Arg	Gly
Asp	His	Val 195	Lys	His	Tyr	Lys	Ile 200	Arg	Lys	Leu	Asp	Met 205	Gly	Gly	Tyr
Tyr	Ile 210	Thr	Thr	Arg	Val	Gln 215	Phe	Asn	Ser	Val	Gln 220	Glu	Leu	Val	Gln
His 225	Tyr	Met	Glu	Val	Asn 230	Asp	Gly	Leu	Cys	Asn 235	Leu	Leu	Ile	Ala	Pro 240
Cys	Thr	Ile	Met	Lys 245	Pro	Gln	Thr	Leu	Gly 250	Leu	Ala	Lys	Asp	Ala 255	Trp
Glu	Ile	Ser	Arg 260	Ser	Ser	Ile	Thr	Leu 265	Glu	Arg	Arg	Leu	Gly 270	Thr	Gly
Cys	Phe	Gly 275	Asp	Val	Trp	Leu	Gly 280	Thr	Trp	Asn	Gly	Ser 285	Thr	Lys	Val
Ala	Val 290	Lys	Thr	Leu	Lys	Pro 295	Gly	Thr	Met	Ser	Pro 300	Lys	Ala	Phe	Leu
Glu 305	Glu	Ala	Gln	Val	Met 310	Lys	Leu	Leu	Arg	His 315	Asp	Lys	Leu	Val	Gln 320
Leu	Tyr	Ala	Val	Val 325	Ser	Glu	Glu	Pro	Ile 330	Tyr	Ile	Val	Gln	Glu 335	Phe
Met	Cys	His	Gly 340	Ser	Leu	Leu	Asp	Phe 345	Leu	Lys	Asn	Pro	Glu 350	Gly	Gln

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu

360 355 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg . 380 370 375

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 475

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 520 515

Thr

<210> 11

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fgr-YF

<400> 11

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys 10

Glu	Asp	Ala	Gly 20	Leu	Glu	Gly	Asp	Phe 25	Arg	Ser	Tyr	Gly	Ala 30	Ala	Asp
His	Tyr	Gly 35	Pro	Asp	Pro	Thr	Lys 40	Ala	Arg	Pro	Ala	Ser 45	Ser	Phe	Ala
His	Ile 50	Pro	Asn	Tyr	Ser	Asn 55	Phe	Ser	Ser	Gln	Ala 60	Ile	Asn	Pro	Gly
Phe 65	Leu	Asp	Ser	Gly	Thr 70	Ile	Arg	Gly	Val	Ser 75	Gly	Ile	Gly	Val	Thr 80
Leu	Phe	Ile	Ala	Leu 85	Tyr	Asp	Tyr	Glu	Ala 90	Arg	Thr	Glu	Asp	Asp 95	Leu
Thr	Phe	Thr	Lys 100	Gly	Glu	Lys	Phe	His 105	Ile	Leu	Asn	Asn	Thr 110	Glu	Gly
Asp	Trp	Trp 115	Glu	Ala	Arg	Ser	Leu 120	Ser	Ser	Gly	Lys	Thr 125	Gly	Cys	Ile
Pro	Ser 130	Asn	Tyr	Val	Ala	Pro 135	Val	Asp	Ser	Ile	Gln 140	Ala	Glu	Glu	Trp
Tyr 145	Phe	Gly	Lys	Ile	Gly 150	Arg	Lys	Asp	Ala	Glu 155	Arg	Gln	Leu	Leu	Ser 160
Pro	Gly	Asn	Pro	Gln 165	Gly	Ala	Phe	Leu	Ile 170	Arg	Glu	Ser	Glu	Thr 175	Thr
Lys	Gly	Ala	Tyr 180	Ser	Leu	Ser	Ile	Arg 185	Asp	Trp	Asp	Gln	Thr 190	Arg	Gly
Asp	His	Val 195	Lys	His	Tyr	Lys	Ile 200	Arg	Lys	Leu	Asp	Met 205	Gly	Gly	Tyr
Tyr	Ile 210	Thr	Thr	Arg	Val	Gln 215	Phe	Asn	Ser	Val	Gln 220	Glu	Leu	Val	Gln
His 225	Tyr	Met	Glu	Val	Asn 230	Asp	Gly	Leu	Суз	Asn 235	Leu	Leu	Ile	Ala	Pro 240
Cys	Thr	Ile	Met	Lys 245	Pro	Gln	Thr	Leu	Gly 250	Leu	Ala	Lys	Asp	Ala 255	Trp

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly

265

260

											20/1	,,			
Cys	Phe	Gly 275	Asp	Val	Trp	Leu	Gly 280	Thr	Trp	Asn	Gly	Ser 285	Thr	Lys	Val
Ala	Val 290		Thr	Leu	Lys	Pro 295		Thr	Met	Ser	Pro 300		Ala	Phe	Leu
Glu 305	Glu	Ala	Gln	Val	Met 310	Lys	Leu	Leu	Arg	His 315	Asp	Lys	Leu	Val	Gln 320
Leu	Tyr	Ala	Val	Val 325	Ser	Glu	Glu	Pro	Ile 330	Tyr	Ile	Val	Thr	Glu 335	Phe
Met	Cys	His	Gly 340	Ser	Leu	Leu	Asp	Phe 345	Leu	Lys	Asn	Pro	Glu 350	Gly	Gln
Asp	Leu	Arg 355	Leu	Pro	Gln	Leu	Val 360	Asp	Met	Ala	Ala	Gln 365	Val	Ala	Glu
Gly	Met 370	Ala	Tyr	Met	Glu	Arg 375	Met	Asn	Tyr	Ile	His 380	Arg	Asp	Leu	Arg
Ala 385	Ala	Asn	Ile	Leu	Val 390	Gly	Glu	Arg	Leu	Ala 395	Cys	Lys	Ile	Ala	Asp 400
Phe	Gly	Leu	Ala	Arg 405	Leu	Ile	Lys	Asp	Asp 410	Glu	Tyr	Asn	Pro	Cys 415	
Gly	Ser	Lys	Phe 420	Pro	Ile	Lys	Trp	Thr 425	Ala	Pro	Glu	Ala	Ala 430	Leu	Phe
Gly	Arg	Phe 435	Thr	Ile	Lys	Ser	Asp 440	Val	Trp	Ser	Phe	Gly 445	Ile	Leu	Leu
	Glu 450		Ile		-	455	-				460				
465			Leu		470					475					480
			Pro	485					490					495	
Lou	F		500	Jau	9	110	****	505	-	-1-			510		

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln 515 520525

WO 2005/059168 PCT/EP2004/053321

Thr

<210> 12

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fgr-TQ/YF

<400> 12

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
1 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45

His Tle Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly

			180					185					190		
Asp	His	Val 195	ГÀг	His	Tyr	Lys	Ile 200	Arg	Lys	Leu	Asp	Met 205	Gly	Gly	Tyr
Tyr	Ile 210	Thr	Thr	Arg	Val	Gln 215	Phe	Asn	Ser	Val	Gln 220	Glu	Leu	Val	Gln
His 225	Tyr	Met	Glu	Val	Asn 230	Asp	Gly	Leu	Cys	Asn 235	Leu	Leu	Ile	Ala	Pro 240
Cys	Thr	Ile	Met	Lys 245	Pro	Gln	Thr	Leu	Gly 250	Leu	Ala	Lys	Asp	Ala 255	Trp
Glu	Ile	Ser	Arg 260	Ser	Ser	Ile	Thr	Leu 265	Glu	Arg	Arg	Leu	Gly 270	Thr	Gly
Cys	Phe	Gly 275	Asp	Val	Trp	Leu	Gly 280	Thr	Trp	Asn	Gly	Ser 285	Thr	Lys	Val
Ala	Val 290	Lys	Thr	Leu	Lys	Pro 295	Gly	Thr	Met	Ser	Pro 300	Lys	Ala	Phe	Leu
Glu 305	Glu	Ala	Gln	Val	Met 310	Lys	Leu	Leu	Arg	His 315	Asp	Lys	Leu	Val	Gln 320
Leu	Tyr	Ala	Val	Val 325	Ser	Glu	Glu	Pro	Ile 330	Tyr	Ile	Val	Gln	Glu 335	Phe
Met	Cys	His	Gly 340	Ser	Leu	Leu	Asp	Phe 345	Leu	Lys	Asn	Pro	Glu 350	Gly	Gln
Asp	Leu	Arg 355	Leu	Pro	Gln	Leu	Val 360	Asp	Met	Ala	Ala	Gln 365	Val	Ala	Glu
Gly	Met 370	Ala	Tyr	Met	Glu	Arg 375	Met	Asn	Tyr	Ile	His 380	Arg	Asp	Leu	Arg
Ala 385	Ala	Asn	Ile	Leu	Val 390	Gly	Glu	Arg	Leu	Ala 395	Cys	Lys	Ile	Ala	Asp 400
Phe	Gly	Leu	Ala	Arg 405	Leu	Ile	Lys	Asp	Asp 410	Glu	Tyr	Asn	Pro	Cys 415	Gln
Gly	Ser	Lys	Phe 420	Pro	Ile	Lys	Trp	Thr 425	Ala	Pro	Glu	Ala	Ala 430	Leu	Phe

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Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln 515 520 525

Thr

<210> 13

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fyn-KA

<400> 13

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg 85 90 95

T	hr	Glu	Asp	Asp 100	Leu	Ser	Phe	His	Lys 105	Gly	Glu	Lys	Phe	Gln 110	Ile	Leu
A	sn	Ser	Ser 115	Glu	Gly	Asp	Trp	Trp 120	Glu	Ala	Arg	Ser	Leu 125	Thr	Thr	Gly
G	lu	Thr 130	Gly	Tyr	Ile	Pro	Ser 135	Asn	Tyr	Val	Ala	Pro 140	Val	Asp	Ser	Ile
	ln 45	Ala	Glu	Glu	Trp	Tyr 150	Phe	Gly	Lys	Leu	Gly 155	Arg	Lys	Asp	Ala	Glu 160
A	rg	Gln	Leu	Leu	Ser 165	Phe	Gly	Asn	Pro	Arg 170	Gly	Thr	Phe	Leu	Ile 175	Arg
G	lu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp
A	.sp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	Lys	Leu
A	.sp	Asn 210	Gly	Gly	Tyr	Tyr	Ile 215	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu
	1n 25	Gln	Leu	Val	Gln	His 230	Tyr	Ser	Glu	Arg	Ala 235	Ala	Gly	Leu	Cys	Cys 240
A	.rg	Leu	Val	Val	Pro 245	Cys	His	Lys	Gly	Met 250	Pro	Arg	Leu	Thr	Asp 255	Leu
s	er	Val	Lys	Thr 260	Lys	Asp	Val	Trp	Glu 265	Ile	Pro	Arg	Glu	Ser 270	Leu	Gln
L	eu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly
Т	hr	Trp 290	Asn	Gly	Asn	Thr	Lys 295	Val	Ala	Ile	Ala	Thr 300	Leu	Lys	Pro	Gly
	hr 05	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320
L	eu	Lys	His	Asp	Lys 325	Leu	Val	Gln	Leu	Tyr 330	Ala	Val	Val	Ser	Glu 335	Glu
P	ro	Ile	Tyr	Ile 340	Val	Thr	Glu	Tyr	Met 345	Asn	Lys	Gly	Ser	Leu 350	Leu	Asp

345

350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 360

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 375

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 395 390

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu 410

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp 425

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 470

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His 485

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 505 500

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 520 515

Pro Gln Tyr Gln Pro Gly Glu Asn Leu 535 530

<210> 14

<211> 537 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fyn-TQ

<400> 14

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu

											32/1	03			
1				5					10					15	
Glu	Arg	Asp	Gly 20	Ser	Leu	Asn	Gln	Ser 25	Ser	Gly	Tyr	Arg	Tyr 30	Gly	Thr
Asp	Pro	Thr 35	Pro	Gln	His	Tyr	Pro 40	Ser	Phe	Gly	Val	Thr 45	Ser	Ile	Pro
Asn	Tyr 50	Asn	Asn	Phe	His	Ala 55	Ala	Gly	Gly	Gln	Gly 60	Leu	Thr	Val	Phe
Gly 65	Gly	Val	Asn	Ser	Ser 70	Ser	His	Thr	Gly	Thr 75	Leu	Arg	Thr	Arg	Gly 80
Gly	Thr	Gly	Val	Thr 85	Leu	Phe	Val	Ala	Leu 90	Tyr	Asp	Tyr	Glu	Ala 95	Arg
Thr	Glu	Asp	Asp 100	Leu	Ser	Phe	His	Lys 105	Gly	Glu	Lys	Phe	Gln 110	Ile	Leu
Asn	Ser	Ser 115	Glu	Gly	Asp	Trp	Trp 120	Glu	Ala	Arg	Ser	Leu 125	Thr	Thr	Gly
Glu	Thr 130	Gly	Tyr	Ile	Pro	Ser 135	Asn	Tyr	Val	Ala	Pro 140	Val	Asp	Ser	Ile
Gln 145	Ala	Glu	Glu	Trp	Tyr 150	Phe	Gly	Lys	Leu	Gly 155	Arg	Lys	Asp	Ala	Glu 160
Arg	Gln	Leu	Leu	Ser 165	Phe	Gly	Asn	Pro	Arg 170	Gly	Thr	Phe	Leu	Ile 175	Arg
Glu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp
Asp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	Lys	Leu
Asp	Asn 210	Gly	Gly	Tyr	Tyr	Ile 215	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu

250

495

510

											33/1	03			
Ser	Val	Lys	Thr 260	Lys	Asp	Val	Trp	Glu 265	Ile	Pro	Arg	Glu	Ser 270	Leu	Gln
Leu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly
Thr	Trp 290	Asn	Gly	Asn	Thr	Lys 295	Val	Ala	Ile	Lys	Thr 300	Leu	Lys	Pro	Gly
Thr 305	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320
Leu	Lys	His	Asp	Lуs 325	Leu	Val	Gln	Leu	Tyr 330	Ala	Val	Val	Ser	Glu 335	Glu
Pro	Ile	Tyr	Ile 340	Val	Gln	Glu	Tyr	Met 345	Asn	Lys	Gly	Ser	Leu 350	Leu	Asp
Phe	Leu	Lys 355	Asp	Gly	Glu	Gly	Arg 360	Ala	Leu	Lys	Leu	Pro 365	Asn	Leu	Val
Asp	Met 370	Ala	Ala	Gln	Val	Ala 375	Ala	Gly	Met	Ala	Tyr 380	Ile	Glu	Arg	Met
Asn 385	Tyr	Ile	His	Arg	Asp 390	Leu	Arg	Ser	Ala	Asn 395	Ile	Leu	Val	Gly	Asn 400
Gly	Leu	Ile	Cys	Lys 405	Ile	Ala	Asp	Phe	Gly 410	Leu	Ala	Arg	Leu	Ile 415	Glu
Asp	Asn	Glu	Tyr 420	Thr	Ala	Arg	Gln	Gly 425	Ala	Lys	Phe	Pro	Ile 430	Lys	Trp
Thr	Ala	Pro 435	Glu	Ala	Ala	Leu	Tyr 440	Gly	Arg	Phe	Thr	Ile 445	Lys	Ser	Asp
Val	Trp. 450	Ser	Phe	Gly	Ile	Leu 455	Leu	Thr	Glu	Leu	Val 460	Thr	Lys	Gly	Arg
Val 465	Pro	Tyr	Pro	Gly	Met 470	Asn	Asn	Arg	Glu	Val 475	Leu	Glu	Gln	Val	Glu 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr

505

485

500

34/103

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 535

<210> 15

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fyn-YF

<400> 15

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Gly Gly Gly Gly Leu Thr Val Phe 50 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly 115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 130 140

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu 195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu 210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys 225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu 245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu 325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp \$340\$

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp

. 36/103

420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Glu Val Glu 465 470 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Phe Gln Pro Gly Glu Asn Leu 530 535

<210> 16

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Fyn-TQ/YF

<400> 16

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly 120

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 135

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 150

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 170

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 185

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu 200

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu 215

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys 230 235

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Ser Glu Glu 325 330

Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415 \hspace{1.5cm}$

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp 420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Phe Gln Pro Gly Glu Asn Leu 530 535

<210> 17

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lck-KA

<400> 17

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His 195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val 225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe

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250 255 245 Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val 260 265 Ala Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu 275 280 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu 305 310 315 320 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 330 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 345 Ala Phe Ile Glu Glu Arq Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 360 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly 375 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 390 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 440 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 455 460 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 470 475 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp

490

485

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro 500 505

<210> 18

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lck-TQ

<400> 18

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 150 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 180 185 190

Ile	Ser	Pro 195	Arg	Ile	Thr	Phe	Pro 200	Gly	Leu	His	Glu	Leu 205	Val	Arg	His
Tyr	Thr 210	Asn	Ala	Ser	Asp	Gly 215	Leu	Cys	Thr	Arg	Leu 220	Ser	Arg	Pro	Cys
Gln 225	Thr	Gln	Lys	Pro	Gln 230	Lys	Pro	Trp	Trp	Glu 235	Asp	Glu	Trp	Glu	Val 240
Pro	Arg	Glu	Thr	Leu 245	Lys	Leu	Val	Glu	Arg 250	Leu	Gly	Ala	Gly	Gln 255	Phe
Gly	Glu	Val	Trp 260	Met	Gly	Tyr	Tyr	Asn 265	Gly	His	Thr	Lys	Val 270	Ala	Val
Lys	Ser	Leu 275	Lys	Gln	Gly	Ser	Met 280	Ser	Pro	Asp	Ala	Phe 285	Leu	Ala	Glu
Ala	Asn 290	Leu	Met	Lys	Gln	Leu 295	Gln	His	Gln	Arg	Leu 300	Val	Arg	Leu	Tyr
Ala 305	Val	Val	Thr	Gln	Glu 310	Pro	Ile	Tyr	Ile	Ile 315	Gln	Glu	Tyr	Met	Glu 320
Asn	Gly	Ser	Leu	Val 325	Asp	Phe	Leu	Lys	Thr 330	Pro	Ser	Gly	Ile	Lуs 335	Leu
Thr	Ile	Asn	Lys 340	Leu	Leu	Asp	Met	Ala 345	Ala	Gln	Ile	Ala	Glu 350	Gly	Met
Ala	Phe	Ile 355	Glu	Glu	Arg	Asn	Tyr 360	Ile	His	Arg	Asp	Leu 365	Arg	Ala	Ala
Asn	Ile 370	Leu	Val	Ser	Asp	Thr 375	Leu	Ser	Cys	Lys	Ile 380	Ala	Asp	Phe	Gly
Leu 385	Ala	Arg	Leu	Ile	Glu 390	Asp	Asn	Glu	Tyr	Thr 395	Ala	Arg	Glu	Gly	Ala 400
Lys	Phe	Pro	Ile	Lys 405	Trp	Thr	Ala	Pro	Glu 410	Ala	Ile	Asn	Tyr	Gly 415	Thr
Phe	Thr	Ile	Lys 420	Ser	Asp	Val	Trp	Ser 425	Phe	Gly	Ile	Leu	Leu 430	Thr	Glu
					_		_	_					_	_	01

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 455

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 470 475

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 490

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro

<210> 19

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lck-YF

<400> 19

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 70

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro

44	1-4	^	~
4.4	. /	11	•

380

135 140 130 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 150 155 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 185 190 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His 200 205 Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu 280 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr 295 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu 315 310 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 330 325 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 340 345 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 360 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly

375

370

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro 500

<210> 20

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lck-TQ/YF

<400> 20

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly	Phe	Glu	Lys	Gly 85	Glu	Pro	Leu	Arg	Ile 90	Leu	Glu	Gln	Ser	Gly 95	Glu
Trp	Trp	Lys	Ala 100	Gln	Ser	Leu	Thr	Thr 105	Gly	Gln	Glu	Gly	Phe 110	Ile	Pro
Phe	Asn	Phe 115	Val	Ala	Lys	Ala	Asn 120	Ser	Leu	Glu	Pro	Glu 125	Pro	Trp	Phe
Phe	Lys 130	Asn	Leu	Ser	Arg	Lys 135	Asp	Ala	Glu	Arg	Gln 140	Leu	Leu	Ala	Pro
Gly 145	Asn	Thr	His	Gly	Ser 150	Phe	Leu	Ile	Arg	Glu 155	Ser	Glu	Ser	Thr	Ala 160
Gly	Ser	Phe	Ser	Leu 165	Ser	Val	Arg	Asp	Phe 170	Asp	Gln	Asn	Gln	Gly 175	Glu
Val	Val	Lys	His 180	Tyr	Lys	Ile	Arg	Asn 185	Leu	Asp	Asn	Gly	Gly 190	Phe	Tyr
Ile	Ser	Pro 195	Arg	Ile	Thr	Phe	Pro 200	Gly	Leu	His	Glu	Leu 205	Val	Arg	His
Tyr	Thr 210	Asn	Ala	Ser	Asp	Gly 215	Leu	Cys	Thr	Arg	Leu 220	Ser	Arg	Pro	Cys
Gln 225	Thr	Gln	Lys	Pro	Gln 230	Lys	Pro	Trp	Trp	Glu 235	Asp	Glu	Trp	Glu	Val 240
Pro	Arg	Glu	Thr	Leu 245	Lys	Leu	Val	Glu	Arg 250	Leu	Gly	Ala	Gly	Gln 255	Phe
Gly	Glu	Val	Trp 260	Met	Gly	Tyr	Tyr	Asn 265	Gly	His	Thr	Lys	Val 270	Ala	Val
Lys	Ser	Leu 275	Lys	Gln	Gly	Ser	Met 280	Ser	Pro	Asp	Ala	Phe 285	Leu	Ala	Glu
Ala	Asn 290	Leu	Met	Lys	Gln	Leu 295	Gln	His	Gln	Arg	Leu 300	Val	Arg	Leu	Tyr
Ala 305	Val	Val	Thr	Gln	Glu 310	Pro	Ile	Tyr	Ile	Ile 315	Gln	Glu	Tyr	Met	Glu 320
Asn	Gly	Ser	Leu	Val 325	Asp	Phe	Leu	Lys	Thr 330	Pro	Ser	Gly	Ile	Lys 335	Leu

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly 370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro 500 505

<210> 21

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Hck-KA

<400> 21

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu 1 $$ 5 $$ 10 $$ 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly

48/	1	C

25 20 30 Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 40 Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 55 His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile 70 Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu 105 100 Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125 Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 135 Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys 170 Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 200 Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His 215 Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys 235 230 Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile 245 250 Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe

265

260

		49/
6		49/

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val 280 Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His 310 315

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala 330

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 345

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 375

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 425 420

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu 440 435

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu 460 450 455

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 475 480 470

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 515 520 525

<210> 22 <211> 525 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Description of sequence: Hck-TQ <400> 22 Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu 1 5 10 Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly 20 25 30 Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 40 Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 120 Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 135 Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 155 150 Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys 165 170 Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp 180

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 195 200 205

Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
Tyr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Cys	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	Lys	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Ala	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu
Ala 305	Asn	Val	Met	Lys	Thr 310	Leu	Gln	His	Asp	Lys 315	Leu	Val	Lys	Leu	His 320
Ala	Val	Val	Thr	Lys 325	Glu	Pro	Ile	Tyr	Ile 330	Ile	Gln	Glu	Phe	Met 335	Ala
Lys	Gly	Ser	Leu 340	Leu	Asp	Phe	Leu	Lys 345	Ser	Asp	Glu	Gly	Ser 350	Lys	Gln
Pro	Leu	Pro 355	Lys	Leu	Ile	Asp	Phe 360	Ser	Ala	Gln	Ile	Ala 365	Glu	Gly	Met
Ala	Phe 370	Ile	Glu	Gln	Arg	Asn 375	Tyr	Ile	His	Arg	Asp 380	Leu	Arg	Ala	Ala
Asn 385	Ile	Leu	Val	Ser	Ala 390	Ser	Leu	Val	Cys	Lys 395	Ile	Ala	Asp	Phe	Gly 400
Leu	Ala	Arg	Val	Ile 405	Glu	Asp	Asn	Glu	Tyr 410	Thr	Ala	Arg	Glu	Gly 415	Ala
Lys	Phe	Pro	Ile 420	Lys	Trp	Thr	Ala	Pro 425	Glu	Ala	Ile	Asn	Phe 430	Gly	Ser
Phe	Thr	Ile 435	Lys	Ser	Asp	Val	Trp 440	Ser	Phe	Gly	Ile	Leu 445	Leu	Met	Glu

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu

450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 515 520 525

<210> 23

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Hck-YF

<400> 23

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu 1 $$ 5 $$ 10 $$ 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125

	-	51	DCL DCG GEG 1	nr Glu Glu Trp Phe
130 135 140	.30	135	1	40

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys 165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp 180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His 210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys 225 230 230 235

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile 245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe 260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val 275 280 285

Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu 290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His 305 310 315

Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala 325 330 335

Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 340 345 350

Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met 355 360 365

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 370 375 380

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly 385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu 435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu 450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro 515 520 525

<210> 24

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Hck-TQ/YF

<400> 24

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu 1 $$ 5 $$ 10 $$ 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 55

His 65	Asn	Ser	Asn	Thr	Pro 70	Gly	Ile	Arg	Glu	Ala 75	Gly	Ser	Glu	Asp	Ile 80
Ile	Val	Val	Ala	Leu 85	Tyr	Asp	Tyr	Glu	Ala 90	Ile	His	His	Glu	Asp 95	Leu
Ser	Phe	Gln	Lys 100	Gly	Asp	Gln	Met	Val 105	Val	Leu	Glu	Glu	Ser 110	Gly	Glu
Trp	Trp	Lys 115	Ala	Arg	Ser	Leu	Ala 120	Thr	Arg	Lys	Glu	Gly 125	Tyr	Ile	Pro
Ser	Asn 130	Tyr	Val	Ala	Arg	Val 135	Asp	Ser	Leu	Glu	Thr 140	Glu	Glu	Trp	Phe
Phe 145	Lys	Gly	Ile	Ser	Arg 150	Lys	Asp	Ala	Glu	Arg 155	Gln	Leu	Leu	Ala	Pro 160
Gly	Asn	Met	Leu	Gly 165	Ser	Phe	Met	Ile	Arg 170	Asp	Ser	Glu	Thr	Thr 175	Lys
Gly	Ser	Tyr	Ser 180	Leu	Ser	Val	Arg	Asp 185	Tyr	Asp	Pro	Arg	Gln 190	Gly	Asp
Thr	Val	Lys 195	His	Tyr	Lys	Ile	Arg 200	Thr	Leu	Asp	Asn	Gly 205	Gly	Phe	Tyr
Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
Tyr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Cys	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	Lys	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Lys	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His

315 320 305 310 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Gln Glu Phe Met Ala 325 330 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 340 345 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met 355 360 365 Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 375 Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly 385 390 395 Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 425 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 470 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg 490 Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Pro 520 515 <210> 25 <211> 511 <212> PRT <213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lyn-KA

<400> 25

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 90 . 95

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His 165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly 180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys 210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 225 230 235 240

Glu :	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly
Gln 1	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val
Ala	Val	Ala 275	Thr	Leu	Lys	Pro	Gly 280	Thr	Met	Ser	Val	Gln 285	Ala	Phe	Leu
Glu	Glu 290	Ala	Asn	Leu	Met	Lys 295	Thr	Leu	Gln	His	Asp 300	Lys	Leu	Val	Arg
Leu '	Tyr	Ala	Val	Val	Thr 310	Arg	Glu	Glu	Pro	Ile 315	Tyr	Ile	Ile	Thr	Glu 320
Tyr l	Met	Ala	Lys	Gly 325	Leu	Leu	Asp	Phe	Leu 330	Lys	Ser	Asp	Glu	Gly 335	Gly
Lys '	Val	Leu	Leu 340	Pro	Lys	Leu	Ile	Asp 345	Phe	Ser	Ala	Gln	Ile 350	Ala	Glu
Gly 1	Met	Ala 355	Tyr	Ile	Glu	Arg	Lys 360	Asn	Tyr	Ile	His	Arg 365	Asp	Leu	Arg
Ala	Ala 370	Asn	Val	Leu	Val	Ser 375	Glu	Ser	Leu	Met	Cys 380	Lys	Ile	Ala	Asp
Phe (Gly	Leu	Ala	Arg	Val 390	Ile	Glu	Asp	Asn	Glu 395	Tyr	Thr	Ala	Arg	Glu 400
Gly :	Ala	Lys	Phe	Pro 405	Ile	Lys	Trp	Thr	Ala 410	Pro	Glu	Ala	Ile	Asn 415	Phe
Gly	Суз	Phe	Thr 420	Ile	Lys	Ser	Asp	Val 425	Trp	Ser	Phe	Gly	Ile 430	Leu	Leu
Tyr	Glu	Ile 435	Val	Thr	Tyr	Gly	Lys 440	Ile	Pro	Tyr	Pro	Gly 445	Arg	Thr	Asn
Ala	Asp 450	Val	Met	Thr	Ala	Leu 455	Ser	Gln	Gly	Tyr	Arg 460	Met	Pro	Arg	Val
Glu 2 465	Asn	Cys	Pro	Asp	Glu 470	Leu	Tyr	Asp	Ile	Met 475	Lys	Met	Cys	Trp	Lys 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro 500 505 510

<210> 26

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lyn-TQ

<400> 26

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly

60/1

185 190 180 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 225 230 235 240 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly 245 250 255 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 260 265 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 275 280 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg 295 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 345 Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 360 Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 375 Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 390 395 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro 500 505 510

<210> 27

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Lyn-YF

<400> 27

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125

Trp	Phe 130	Phe	Lys	Asp	Ile	Thr 135	Arg	Lys	Asp	Ala	Glu 140	Arg	Gln	Leu	Leu
Ala 145	Pro	Gly	Asn	Ser	Ala 150	Gly	Ala	Phe	Leu	Ile 155	Arg	Glu	Ser	Glu	Thr 160
Leu	Lys	Gly	Ser	Phe 165	Ser	Leu	Ser	Val	Arg 170	Asp	Phe	Asp	Pro	Val 175	His
Gly	Asp	Val	Ile 180	Lys	His	Tyr	Lys	Ile 185	Arg	Ser	Leu	Asp	Asn 190	Gly	Gly
Tyr	Tyr	Ile 195	Ser	Pro	Arg	Ile	Thr 200	Phe	Pro	Cys	Ile	Ser 205	Asp	Met	Ile
Lys	His 210	Tyr	Gln	Lys	Gln	Ala 215	Asp	Gly	Leu	Cys	Arg 220	Arg	Leu	Glu	Lys
Ala 225	Cys	Ile	Ser	Pro	Lys 230	Pro	Gln	Lys	Pro	Trp 235	Asp	Lys	Asp	Ala	Trp 240
Glu	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly
Gln	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val
Ala	Val	Lys 275	Thr	Leu	Lys	Pro	Gly 280	Thr	Met	Ser	Val	Gln 285	Ala	Phe	Leu
Glu	Glu 290	Ala	Asn	Leu	Met	Lys 295	Thr	Leu	Gln	His	Asp 300	Lys	Leu	Val	Arg
Leu 305	Tyr	Ala	Val	Val	Thr 310	Arg	Glu	Glu	Pro	Ile 315	Tyr	Ile	Ile	Thr	Glu 320
Tyr	Met	Ala	Lys	Gly 325	Leu	Leu	Asp	Phe	Leu 330	Lys	Ser	Asp	Glu	Gly 335	Gly
Lys	Val	Leu	Leu 340	Pro	Lys	Leu	Ile	Asp 345	Phe	Ser	Ala	Gln	Ile 350	Ala	Glu
Gly	Met	Ala 355	Tyr	Ile	Glu	Arg	Lys 360	Asn	Tyr	Ile	His	Arg 365	Asp	Leu	Arg
Ala	Ala 370	Asn	Val	Leu	Val	Ser 375	Glu	Ser	Leu	Met	Cys 380	Lys	Ile	Ala	Asp

Phe 385	Gly	Leu	Ala	_	Val 390	Ile	Glu	Asp	Asn	Glu 395	Tyr	Thr	Ala	Arg	Glu 400

- Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe 405 410 415
- Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430
- Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445
- Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460
- Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475 480
- Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495
- Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Gln Pro 500 505 510
- <210> 28
- <211> 511
- <212> PRT
- <213> Homo sapiens
- <220>
- <221> misc_feature
- <223> Description of sequence: Lyn-TQ/YF
- <400> 28
- Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly 1 5 10 15
- Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30
- Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45
- Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60
- Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp

6					70					75					80
65					70					75					00
Asp	Leu	Ser	Phe	Lys 85	Lys	Gly	Glu	Lys	Met 90	Lys	Val	Leu	Glu	Glu 95	His
Gly	Glu	Trp	Trp 100	Lys	Ala	Lys	Ser	Leu 105	Leu	Thr	Lys	Lys	Glu 110	Gly	Phe
Ile	Pro	Ser 115	Asn	Tyr	Val	Ala	Lys 120	Leu	Asn	Thr	Leu	Glu 125	Thr	Glu	Glu
Trp	Phe 130	Phe	Lys	Asp	Ile	Thr 135	Arg	Lys	Asp	Ala	Glu 140	Arg	Gln	Leu	Leu
Ala 145	Pro	Gly	Asn	Ser	Ala 150	Gly	Ala	Phe	Leu	Ile 155	Arg	Glu	Ser	Glu	Thr 160
Leu	Lys	Gly	Ser	Phe 165	Ser	Leu	Ser	Val	Arg 170	Asp	Phe	Asp	Pro	Val 175	His
Gly	Asp	Val	Ile 180	Lys	His	Tyr	Lys	Ile 185	Arg	Ser	Leu	Asp	Asn 190	Gly	Gly
Tyr	Tyr	Ile 195	Ser	Pro	Arg	Ile	Thr 200	Phe	Pro	Cys	Ile	Ser 205	Asp	Met	Ile
Lys	His 210	Tyr	Gln	Lys	Gln	Ala 215	Asp	Gly	Leu	Cys	Arg 220	Arg	Leu	Glu	Lys
Ala 225	Cys	Ile	Ser	Pro	Lys 230	Pro	Gln	Lys	Pro	Trp 235	Asp	Lys	Asp	Ala	Trp 240
Glu	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly
Gln	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val
Ala	Val	Lys 275	Thr	Leu	Lys	Pro	Gly 280	Thr	Met	Ser	Val	Gln 285	Ala	Phe	Leu
Glu	Glu 290	Ala	Asn	Leu	Met	Lys 295	Thr	Leu	Gln	His	Asp 300	Lys	Leu	Val	Arg
_	-	- 1			m.	_	Q1	~ 1	_		_	- 3	71.	01	C1

Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu

315

310

305

	65/	1

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly 330 325

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 345

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 360

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 375

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 395 390

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 440

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 470

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Gln Pro 505 500

<210> 29

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> Description of sequence: BLK-KA

<400> 29

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10

Glu	Lys	Asp	Lys 20	Gly	Gln	Trp	Ser	Pro 25	Leu	Lys	Val	Ser	Ala 30	Gln	Asp
Lys	Asp	Ala 35	Pro	Pro	Leu	Pro	Pro 40	Leu	Val	Val	Phe	Asn 45	His	Leu	Thr
Pro	Pro 50	Pro	Pro	Asp	Glu	His 55	Leu	Asp	Glu	Asp	Lys 60	His	Phe	Val	Val
Ala 65	Leu	Tyr	Asp	Tyr	Thr 70	Ala	Met	Asn	Asp	Arg 75	Asp	Leu	Gln	Met	Leu 80
Lys	Gly	Glu	Lys	Leu 85	Gln	Val	Leu	Lys	Gly 90	Thr	Gly	Asp	Trp	Trp 95	Leu
Ala	Arg	Ser	Leu 100	Val	Thr	Gly	Arg	Glu 105	Gly	Tyr	Val	Pro	Ser 110	Asn	Phe
Val	Ala	Arg 115	Val	Glu	Ser	Leu	Glu 120	Met	Glu	Arg	Trp	Phe 125	Phe	Arg	Ser
Gln	Gly 130	Arg	Lys	Glu	Ala	Glu 135	Arg	Gln	Leu	Leu	Ala 140	Pro	Ile	Asn	Lys
Ala 145	Gly	Ser	Phe	Leu	Ile 150	Arg	Glu	Ser	Glu	Thr 155	Asn	Lys	Gly	Ala	Phe 160
Ser	Leu	Ser	Val	Lys 165	Asp	Val	Thr	Thr	Gln 170	Gly	Glu	Leu	Ile	Lys 175	His
Tyr	Lys	Ile	Arg 180	Суз	Leu	Asp	Glu	Gly 185	Gly	Tyr	Tyr	Ile	Ser 190	Pro	Arg
Ile	Thr	Phe 195	Pro	Ser	Leu	Gln	Ala 200	Leu	Val	Gln	His	Tyr 205	Ser	Lys	Lys
Gly	Asp 210	Gly	Leu	Cys	Gln	Arg 215	Leu	Thr	Leu	Pro	Cys 220	Val	Arg	Pro	Ala
Pro 225	Gln	Asn	Pro	Trp	Ala 230	Gln	Asp	Glu	Trp	Glu 235	Ile	Pro	Arg	Gln	Ser 240
Leu	Arg	Leu	Val	Arg 245	Lys	Leu	Gly	Ser	Gly 250	Gln	Phe	Gly	Glu	Val 255	Trp

Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Ala Thr Leu Lys 260 265 270

	/10	
6/	/	1

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 325 330 335 .

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val\$355\$ \$360\$ \$365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro
505

<211> 505 <212> PRT <213> Homo sapiens <220> <221> misc_feature <223> Description of sequence: BLK-TQ <400> 30 Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 20 25 Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 40 Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 55 Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 75 70 Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 120 Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 135 Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 155 150 Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His 170 165 Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg

185

205

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys

200

180

195

Gly	Asp	Gly	Leu	Cys	Gln	Arg	Leu	Thr	Leu	Pro	Cys	Val	Arg	Pro	Ala
	210					215					220				

- Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser 230 235
- Leu Arq Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp 245 250
- Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys 265
- Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 280
- Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 295
- Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu 310 315
- Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 330 325
- Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
- Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val 360
- Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile
- Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390
- Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala 405 410
- Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 425 420
- Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 440 445 435
- Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 490 485

Thr Glu Arg Gln Tyr Glu Leu Gln Pro 500

<210> 31

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: BLK-YF

<400> 31

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 25

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 40

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 55

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 75

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe 105 100

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 120 115

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 135

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 150 155 145

Ser	Leu	Ser	Val		Asp	Val	Thr	Thr		Gly	Glu	Leu	Ile		His
				165					170					175	
Tyr	Lys	Ile	Arg 180	Cys	Leu	Asp	Glu	Gly 185	Gly	Tyr	Tyr	Ile	Ser 190	Pro	Arg
Ile	Thr	Phe 195	Pro	Ser	Leu	Gln	Ala 200	Leu	Val	Gln	His	Tyr 205	Ser	Lys	Lys
Gly	Asp 210	Gly	Leu	Cys	Gln	Arg 215	Leu	Thr	Leu	Pro	Cys 220	Val	Arg	Pro	Ala
Pro 225	Gln	Asn	Pro	Trp	Ala 230	Gln	Asp	Glu	Trp	Glu 235	Ile	Pro	Arg	Gln	Ser 240
Leu	Arg	Leu	Val	Arg 245	Lys	Leu	Gly	Ser	Gly 250	Gln	Phe	Gly	Glu	Val 255	Trp
Met	Gly	Tyr	Tyr 260	Lys	Asn	Asn	Met	Lys 265	Val	Ala	Ile	Lys	Thr 270	Leu	Lys
Glu	Gly	Thr 275	Met	Ser	Pro	Glu	Ala 280	Phe	Leu	Gly	Glu	Ala 285	Asn	Met	Met
Lys	Ala 290	Leu	Gln	His	Glu	Arg 295	Leu	Val	Arg	Leu	Tyr 300	Ala	Val	Val	Thr
Lys 305	Glu	Pro	Ile	Tyr	Ile 310	Val	Thr	Glu	Tyr	Met 315	Ala	Arg	Gly	Cys	Leu 320
Leu	Asp	Phe	Leu	Lys 325	Thr	Asp	Glu	Gly	Ser 330	Arg	Leu	Ser	Leu	Pro 335	Arg
Leu	Ile	Asp	Met 340	Ser	Ala	Gln	Ile	Ala 345	Glu	Gly	Met	Ala	Tyr 350	Ile	Glu
Arg	Met	Asn 355	Ser	Ile	His	Arg	Asp 360	Leu	Arg	Ala	Ala	Asn 365	Ile	Leu	Val
Ser	Glu 370	Ala	Leu	Cys	Cys	Lys 375	Ile	Ala	Asp	Phe	Gly 380	Leu	Ala	Arg	Ile
Ile 385	Asp	Ser	Glu	Tyr	Thr 390	Ala	Gln	Glu	Gly	Ala 395	Lys	Phe	Pro	Ile	Lys 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala

410 405 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 425 420

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 440 435

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 470 475

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 490 485

Thr Glu Arg Gln Phe Glu Leu Gln Pro 500

<210> 32

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Description of sequence: Blk-TQ/YF

<400> 32

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 20 .

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 40

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 55

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 70

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu 85 90

Ala	Arg	Ser	Leu 100	Val	Thr	Gly	Arg	Glu 105	Gly	Tyr	Val	Pro	Ser 110	Asn	Phe
Val	Ala	Arg 115	Val	Glu	Ser	Leu	Glu 120	Met	Glu	Arg	Trp	Phe 125	Phe	Arg	Ser
Gln	Gly 130	Arg	Lys	Glu	Ala	Glu 135	Arg	Gln	Leu	Leu	Ala 140	Pro	Ile	Asn	Lys
Ala 145	Gly	Ser	Phe	Leu	Ile 150	Arg	Glu	Ser	Glu	Thr 155	Asn	Lys	Gly	Ala	Phe 160
Ser	Leu	Ser	Val	Lys 165	Asp	Val	Thr	Thr	Gln 170	Gly	Glu	Leu	Ile	Lys 175	His
Туг	Lys	Ile	Arg 180	Cys	Leu	Asp	Glu	Gly 185	Gly	Tyr	Tyr	Ile	Ser 190	Pro	Arg
Ile	Thr	Phe 195	Pro	Ser	Leu	Gln	Ala 200	Leu	Val	Gln	His	Tyr 205	Ser	Lys	Lys
Gly	Asp 210	Gly	Leu	Cys	Gln	Arg 215	Leu	Thr	Leu	Pro	Cys 220	Val	Arg	Pro	Ala
Pro 225	Gln	Asn	Pro	Trp	Ala 230	Gln	Asp	Glu	Trp	Glu 235	Ile	Pro	Arg	Gln	Ser 240
Leu	Arg	Leu	Val	Arg 245	Lys	Leu	Gly	Ser	Gly 250	Gln	Phe	Gly	Glu	Val 255	Trp
Met	Gly	Tyr	Tyr 260	Lys	Asn	Asn	Met	Lys 265	Val	Ala	Ile	Lys	Thr 270	Leu	Lys
Glu	Gly	Thr 275	Met	Ser	Pro	Glu	Ala 280	Phe	Leu	Gly	Glu	Ala 285	Asn	Met	Met
Lys	Ala 290	Leu	Gln	His	Glu		Leu	Val	Arg	Leu	Tyr 300	Ala	Val	Val	Thr
Lys 305	Glu	Pro	Ile	Tyr	Ile 310	Val	Gln	Glu	Tyr	Met 315	Ala	Arg	Gly	Cys	Leu 320
Leu	Asp	Phe	Leu	Lys 325	Thr	Asp	Glu	Gly	Ser 330	Arg	Leu	Ser	Leu	Pro 335	Arg
Leu	Ile	Asp	Met 340	Ser	Ala	Gln	Ile	Ala 345	Glu	Gly	Met	Ala	Tyr 350	Ile	Glu

Arg	Met	Asn 355	Ser	Ile	His	Asp 360	Arg	Ala	Ala	Asn 365	Ile	Leu	Val

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro 500 505

<210> 33

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-KA

<400> 33

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45

Asn Phe H 50	is Ala A	Ala Ala	Val 55	Ser	Pro	Pro	Val	Pro 60	Phe	Ser	Gly	Pro
Gly Phe T 65	yr Pro	Cys Asn 70	Thr	Leu	Gln	Ala	His 75	Ser	Ser	Ile	Thr	Gly 80
Gly Gly V		Leu Phe 85	Ile	Ala	Leu	Tyr 90	Asp	Tyr	Glu	Ala	Arg 95	Thr
Glu Asp A	sp Leu 100	Ser Phe	Gln	Lys	Gly 105	Glų	Lys	Phe	His	Ile 110	Ile	Asn
Asn Thr G	lu Gly . .15	Asp Trp		Glu 120	Ala	Arg	Ser	Leu	Ser 125	Ser	Gly	Ala
Thr Gly T	yr Ile	Pro Ser	Asn 135	Tyr	Val	Ala	Pro	Val 140	Asp	Ser	Ile	Gln
Ala Glu G 145	Glu Trp	Tyr Phe 150	Gly	Lys	Ile	Gly	Arg 155	Lys	Asp	Ala	Glu	Arg 160
Gln Leu L		His Gly 165	Asn	Cys	Arg	Gly 170	Thr	Phe	Leu	Ile	Arg 175	Glu
Ser Glu T	Thr Thr 180	Lys Gly	Ala	Tyr	Ser 185	Leu	Ser	Ile	Arg	Asp 190	Trp	Asp
Glu Ala L	ys Gly .95	Asp His		Lys 200	His	Tyr	Lys	Ile	Arg 205	Lys	Leu	Asp
Ser Gly G 210		Tyr Ile	Thr 215					Phe 220	Asp	Thr	Ile	Gln
Gln Leu V 225	al Gln	His Tyr 230	Ile	Glu	Arg	Ala	Ala 235	Gly	Leu	Cys	Cys	Arg 240
Leu Ala V		Cys Pro 245	Lys	Gly	Thr	Pro 250	Lys	Leu	Ala	Asp	Leu 255	Ser
Val Lys T	Chr Lys 260	Asp Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Gln	Leu
Leu Gln L 2	lys Leu 275	Gly Asn	Gly	Gln 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp Asn G	Sly Thr	Thr Lys	Val	Ala	Val	Ala	Thr	Leu	Lys	Pro	Gly	Thr

	290					295					300				
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Glu	Glu	Ala	Gln 315	Ile	Met	Lys	Arg	Leu 320
Arg	His	Asp	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Phe	Met	Ser 345	Gln	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Asp 355	Gly	Asp	Gly	Arg	Tyr 360	Leu	Lys	Leu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ala 375	Gly	Met	Ala	Tyr	Ile 380	Glu	Arg	Met	Asn
Tyr 385	Ile	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Asp	Asn 400
Leu	Val	Cys	Lys	Ile 405	Ala	Asp	Phe	Gly	Leu 410	Ala	Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Phe	Gly 440	Lys	Phe	Thr	Ile	Lys 445	Ser	Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455	Thr	Glu	Leu	Val	Thr 460	Lys	Gly	Arg	Val
Pro 465	Tyr	Pro	Gly	Met	Asn 470	Asn	Arg	Glu	Val	Leu 475	Glu	Gln	Val	Glu	Arg 480
Gly	Tyr	Arg	Met	Gln 485	Cys	Pro	Gly	Gly	Cys 490	Pro	Pro	Ser	Leu	His 495	Asp
Val	Met	Val	Gln 500	Cys	Trp	Lys	Arg	Glu 505	Pro	Glu	Glu	Arg	Pro 510	Thr	Phe
Glu	Tyr	Leu 515	Gln	Ser	Phe	Leu	Glu 520	Asp	Tyr	Phe	Thr	Ala 525	Thr	Glu	Pro
Gln	Tyr 530	Gln	Pro	Gly	Asp	Asn 535	Gln								

<210> 34

<211> 536

<212> PRT <213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-TQ

<400> 34

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 25

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 40

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 75 70

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 105

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200

Ser	Gly 210	Gly	Tyr	Tyr	Ile	Thr 215	Thr	Arg	Ala	Gln	Phe 220	Asp	Thr	Ile	Gln
Gln 225	Leu	Val	Gln	His	Tyr 230	Ile	Glu	Arg	Ala	Ala 235	Gly	Leu	Cys	Cys	Arg 240
Leu	Ala	Val	Pro	Cys 245	Pro	Lys	Gly	Thr	Pro 250	Lys	Leu	Ala	Asp	Leu 255	Ser
Val	Lys	Thr	Lys 260	Asp	Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Gln	Leu
Leu	Gln	Lys 275	Leu	Gly	Asn	Gly	Gln 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Lys	Val 295	Ala	Val	Lys	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Glu	Glu	Ala	Gln 315	Ile	Met	Lys	Arg	Leu 320
Arg	His	Asp	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Gln	Glu	Phe	Met	Ser 345	Gln	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Asp 355	Ġly	Asp	Gly	Arg	Tyr 360	Leu	Lys	Leu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ala 375	Gly	Met	Ala	Tyr	Ile 380	Glu	Arg	Met	Asn
Tyr 385	Ile	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Asp	Asn 400
Leu	Val	Cys	Lys	Ile 405	Ala	Asp	Phe	Gly	Leu 410	Ala	Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Phe	Gly 440	Lys	Phe	Thr	Ile	Lys 445	Ser	Asp	Val

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val

460

450 455

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln 530 535

<210> 35

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-YF

<400> 35

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala

 100	105

		115					120					125			
Thr	Gly 130	Tyr	Ile	Pro	Ser	Asn 135	Tyr	Val	Ala	Pro	Val 140	Asp	Ser	Ile	Gln
Ala 145	Glu	Glu	Trp	Tyr	Phe 150	Gly	Lys	Ile	Gly	Arg 155	Lys	Asp	Ala	Glu	Arg 160
Gln	Leu	Leu	Cys	His 165	Gly	Asn	Cys	Arg	Gly 170	Thr	Phe	Leu	Ile	Arg 175	Glu
Ser	Glu	Thr	Thr 180	Lys	Gly	Ala	Tyr	Ser 185	Leu	Ser	Ile	Arg	Asp 190	Trp	Asp
Glu	Ala	Lys 195	Gly	Asp	His	Val	Lys 200	His	Tyr	Lys	Ile	Arg 205	Lys	Leu	Asp
Ser	Gly 210	Gly	Tyr	Tyr	Ile	Thr 215	Thr	Arg	Ala	Gln	Phe 220	Asp	Thr	Ile	Gln
Gln 225	Leu	Val	Gln	His	Tyr 230	Ile	Glu	Arg	Ala	Ala 235	Gly	Leu	Cys	Суѕ	Arg 240
Leu	Ala	Val	Pro	Cys 245	Pro	Lys	Gly	Thr	Pro 250	Lys	Leu	Ala	Asp	Leu 255	Ser
Val	Lys	Thr	Lys 260	Asp	Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Gln	Leu
Leu	Gln	Lys 275	Leu	Gly	Asn	Gly	Gln 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Lys	Val 295	Ala	Val	Lys	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Glu	Glu	Ala	Gln 315	Ile	Met	Lys	Arg	Leu 320
Arg	His	Asp	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Phe	Met	Ser 345	Gln	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Asp 355	Gly	Asp	Gly	Arg	Tyr 360	Leu	Lys	Leu	Pro	Gln 365	Leu	Val	Asp

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Met Ala Ala Gl
n Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met As
n 370 375 380

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Glu Val Glu Arg 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln 530 535

<210> 36

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc_feature

<223> Description of sequence: Yrk-TQ/YF

<400> 36

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 20 25 30

- Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45
- Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 55 60
- Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80
- Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95
- Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110
- Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115 120 125
- Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135 140
- Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155 160
- Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170 175
- Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190
- Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200 205
- Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln 210 215 220
- Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg 225 230 235 240
- Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser 245 250 255
- Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu 260 265 270
- Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr 275 280 285

${\tt Trp}$	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr
	290					295					300			_	

- Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu 305 310 315 320
- Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335
- Ile Tyr Ile Val Gln Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe 340 345 350
- Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp 355 360 365
- Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn 370 375 380
- Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn 385 390 395 400
- Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405
 410
 415
- Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430
- Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 435 440 445
- Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val 450 455 460
- Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg 465 470 475 480
- Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495
- Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510
- Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln

530

535

<210> 37 <211> 536 <212> PRT <213> Homo sapiens <220> <223> Src kinase (Fig. 18) <220> <221> SITE <222> (298) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (341) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (530) <223> Constant amino acid Y in domain SH1 <400> 37 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe 25 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 90 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 105 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 120 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 190 185

85/103 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 310 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 360 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn 395 390 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 425 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435 440 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp

490

525

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 505

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 520

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Gln Tyr Gln Pro Gly Glu Asn Leu 530 <210> 38 <211> 543 <212> PRT <213> Homo sapiens <220> <223> Yes kinase (Fig. 18) <220> <221> SITE <222> (305) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (348) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (537) <223> Constant amino acid Y in domain SH1 <400> 38 Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 25 20 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 40 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly 55 Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 85 90 Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 105 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp 115 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 135 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 145 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly 170 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly

	180			185					190		
Ala Tyr Ser 195	Leu Ser	Ile Ar	g Asp 200	Trp	Asp	Glu	Ile	Arg 205	Gly	Asp	Asn
Val Lys His 210	Tyr Lys	Ile Arc		Leu	Asp	Asn	Gly 220	Gly	Tyr	Tyr	Ile
Thr Thr Arg 225	Ala Gln	Phe Asp 230	Thr	Leu	Gln	Lys 235	Leu	Val	Lys	His	Tyr 240
Thr Glu His	Ala Asp 245	Gly Le	ı Cys	His	Lys 250	Leu	Thr	Thr	Val	Cys 255	Pro
Thr Val Lys	Pro Gln 260	Thr Gl	n Gly	Leu 265	Ala	Lys	Asp	Ala	Trp 270	Glu	Ile
Pro Arg Glu 275	Ser Leu	Arg Le	ı Glu 280	Val	Lys	Leu	Gly	Gln 285	Gly	Cys	Phe
Gly Glu Val 290	Trp Met	Gly The		Asn	Gly	Thr	Thr 300	Lys	Val	Ala	Ile
Lys Thr Leu 305	Lys Pro	Gly Th: 310	Met	Met	Pro	Glu 315	Ala	Phe	Leu	Gln	Glu 320
Ala Gln Ile	Met Lys 325	Lys Le	ı Arg	His	Asp 330	Lys	Leu	Val	Pro	Leu 335	Tyr
Ala Val Val	Ser Glu 340	Glu Pro	o Ile	Tyr 345	Ile	Val	Thr	Glu	Phe 350	Met	Ser
Lys Gly Ser 355	Leu Leu	Asp Pho	e Leu 360	Lys	Glu	Gly	Asp	Gly 365	Lys	Tyr	Leu
Lys Leu Pro 370	Gln Leu	Val Ası 37		Ala	Ala	Gln	Ile 380	Ala	Asp	Gly	Met
Ala Tyr Ile 385	Glu Arg	Met Ası 390	n Tyr	Ile	His	Arg 395	Asp	Leu	Arg	Ala	Ala 400
Asn Ile Leu	Val Gly 405	Glu Ası	n Leu	Val	Cys 410	Lys	Ile	Ala	Asp	Phe 415	Gly
Leu Ala Arg	Leu Ile 420	Glu Ası	Asn	Glu 425	Tyr	Thr	Ala	Arg	Gln 430	Gly	Ala
Lys Phe Pro 435	Ile Lys	Trp Th	Ala 440	Pro	Glu	Ala	Ala	Leu 445	Tyr	Gly	Arg
Phe Thr Ile 450	Lys Ser	Asp Val		Ser	Phe	Gly	Ile 460	Leu	Gln	Thr	Glu
Leu Val Thr 465	Lys Gly	Arg Va. 470	L Pro	Tyr	Pro	Gly 475	Met	Val	Asn	Arg	Glu 480
Val Leu Glu	Gln Val 485	Glu Ar	g Gly	Tyr	Arg 490	Met	Pro	Cys	Pro	Gln 495	Gly
Cys Pro Glu	Ser Leu 500	His Gl	ı Leu	Met 505	Asn	Leu	Cys	Trp	Lys 510	Lys	Asp
Pro Asp Glu	Arg Pro	Thr Phe	e Glu	Tyr	Ile	Gln	Ser	Phe	Leu	Glu	Asp

515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 540

<210> 39

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> Fyn kinase (Fig. 18)

<220>

<221> SITE

<222> (299)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (342)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (531)

<223> Constant amino acid Y in domain SH1

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Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg \$90\$

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 165 170 175

Glu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp
Asp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	Lys	Leu
Asp	Asn 210	Gly	Gly	Tyr	Tyr	Ile 215	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu
Gln 225	Gln	Leu	Val	Gln	His 230	Tyr	Ser	Glu	Arg	Ala 235	Ala	Gly	Leu	Cys	Cys 240
Arg	Leu	Val	Val	Pro 245	Суѕ	His	Lys	Gly	Met 250	Pro	Arg	Leu	Thr	Asp 255	Leu
Ser	Val	Lys	Thr 260	Lys	Asp	Val	Trp	Glu 265	Ile	Pro	Arg	Glu	Ser 270	Leu	Gln
Leu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly
Thr	Trp 290	Asn	Gly	Asn	Thr	Lys 295	Val	Ala	Ile	Lys	Thr 300	Leu	Lys	Pro	Gly
Thr 305	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320
Leu	Lys	His	Asp	Lys 325	Leu	Val	Gln	Leu	Tyr 330	Ala	Val	Val	Ser	Glu 335	Glu
Pro	Ile	Tyr	Ile 340	Val	Thr	Glu	Tyr	Met 345	Asn	Lys	Gly	Ser	Leu 350	Leu	Asp
Phe	Leu	Lys 355	Asp	Gly	Glu	Gly	Arg 360	Ala	Leu	Lys	Leu	Pro 365	Asn	Leu	Val
Asp	Met 370	Ala	Ala	Gln	Val	Ala 375	Ala	Gly	Met	Ala	Tyr 380	Ile	Glu	Arg	Met
Asn 385	Tyr	Ile	His	Arg	Asp 390	Leu	Arg	Ser	Ala	Asn 395	Ile	Leu	Val	Gly	Asn 400
Gly	Leu	Ile	Cys	Lys 405	Ile	Ala	Asp	Phe	Gly 410	Leu	Ala	Arg	Leu	Ile 415	Glu
Asp	Asn	Glu	Tyr 420	Thr	Ala	Arg	Gln	Gly 425	Ala	Lys	Phe	Pro	Ile 430	Lys	Trp
Thr	Ala	Pro 435	Glu	Ala	Ala	Leu	Tyr 440	Gly	Arg	Phe	Thr	Ile 445	Lys	Ser	Asp
Val	Trp 450	Ser	Phe	Gly	Ile	Leu 455	Leu	Thr	Glu	Leu	Val 460	Thr	Lys	Gly	Arg
Val 465	Pro	Tyr	Pro	Gly	Met 470	Asn	Asn	Arg	Glu	Val 475	Leu	Glu	Gln	Val	Glu 480
Arg	Gly	Tyr	Arg	Met 485	Pro	Cys	Pro	Gln	Asp 490	Cys	Pro	Ile	Ser	Leu 495	His
Glu	Leu	Met	Ile 500	His	Cys	Trp	Lys	Lys 505	Asp	Pro	Glu	Glu	Arg 510	Pro	Thr

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 Pro Gln Tyr Gln Pro Gly Glu Asn Leu 535 <210> 40 <211> 536 <212> PRT <213> Chicken <220> <223> Yrk kinase (Fig. 18) <220> <221> SITE <222> (298) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (341) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (530) <223> Constant amino acid Y in domain SH1 <400> 40 Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 55 Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 105 Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115 120 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu

170

165

Ser	Glu	Thr	Thr 180	Lys	Gly	Ala	Tyr	Ser 185	Leu	Ser	Ile	Arg	Asp 190	Trp	Asp
Glu	Ala	Lys 195	Gly	Asp	His	Val	Lys 200	His	Tyr	Lys	Ile	Arg 205	Lys	Leu	Asp
Ser	Gly 210	Gly	Tyr	Tyr	Ile	Thr 215	Thr	Arg	Ala	Gln	Phe 220	Asp	Thr	Ile	Gln
Gln 225	Leu	Val	Gln	His	Tyr 230	Ile	Glu	Arg	Ala	Ala 235	Gly	Leu	Суз	Cys	Arg 240
Leu	Ala	Val	Pro	Cys 245	Pro	Lys	Gly	Thr	Pro 250	Lys	Leu	Ala	Asp	Leu 255	Ser
Val	Lys	Thr	Lys 260	Asp	Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Gln	Leu
Leu	Gln	Lys 275	Leu	Gly	Asn	Gly	Gln 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Lys	Val 295	Ala	Val	Lys	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Glu	Glu	Ala	Gln 315	Ile	Met	Lys	Arg	Leu 320
Arg	His	Asp	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Phe	Met	Ser 345	Gln	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Asp 355	Gly	Asp	Gly	Arg	Tyr 360	Leu	Lys	Leu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ala 375	Gly	Met	Ala	Tyr	Ile 380	Glu	Arg	Met	Asn
Tyr 385	Ile	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395	Leu	Val	Gly	Asp	Asn 400
Leu	Val	Cys	Lys	Ile 405	Ala	Asp	Phe	Gly	Leu 410	Ala	Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Phe	Gly 440	Lys	Phe	Thr	Ile	Lys 445	Ser	Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455	Thr	Glu	Leu	Val	Thr 460	Lys	Gly	Arg	Val
Pro 465	Tyr	Pro	Gly	Met	Asn 470	Asn	Arg	Glu	Val	Leu 475	Glu	Gln	Val	Glu	Arg 480
Gly	Tyr	Arg	Met	Gln 485	Cys	Pro	Gly	Gly	Cys 490	Pro	Pro	Ser	Leu	His 495	Asp
Val	Met	Val	Gln 500	Cys	Trp	Lys	Arg	Glu 505	Pro	Glu	Glu	Arg	Pro 510	Thr	Phe

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 520 Gln Tyr Gln Pro Gly Asp Asn Gln 530 <210> 41 <211> 529 <212> PRT <213> Homo sapiens <220> <223> Fgr kinase (Fig. 18) <220> <221> SITE <222> (291) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (334) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (523) <223> Constant amino acid Y in domain SH1 Met Gly Cys Val Phe Cys Lys Leu Glu Pro Val Ala Thr Ala Lys Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 40 35 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 55 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105 Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 120 Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 155

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr

	165		170		175
Lys Gly Ala Tyr 180	Ser Leu Ser	Ile Arg 185	Asp Trp Asp	Gln Thr 190	Arg Gly
Asp His Val Lys 195	His Tyr Lys	Ile Arg 200	Lys Leu Asp	Met Gly 205	Gly Tyr
Tyr Ile Thr Thr 210	Arg Val Gln 215	Phe Asn	Ser Val Gln 220	Glu Leu	Val Gln
His Tyr Met Glu 225	Val Asn Asp 230	Gly Leu	Cys Asn Leu 235	Leu Ile	Ala Pro 240
Cys Thr Ile Met	Lys Pro Gln 245	Thr Leu	Gly Leu Ala 250	Lys Asp	Ala Trp 255
Glu Ile Ser Arg 260	Ser Ser Ile	Thr Leu 265	Glu Arg Arg	Leu Gly 270	Thr Gly
Cys Phe Gly Asp 275	Val Trp Leu	Gly Thr 280	Trp Asn Gly	Ser Thr 285	Lys Val
Ala Val Lys Thr 290	Leu Lys Pro 295	Gly Thr	Met Ser Pro 300	Lys Ala	Phe Leu
Glu Glu Ala Gln 305	Val Met Lys 310	Leu Leu	Arg His Asp 315	Lys Leu	Val Gln 320
Leu Tyr Ala Val	Val Ser Glu 325	Glu Pro	Ile Tyr Ile 330	Val Thr	Glu Phe 335
Met Cys His Gly 340	Ser Leu Leu	Asp Phe 345	Leu Lys Asn	Pro Glu 350	Gly Gln
Asp Leu Arg Leu 355	Pro Gln Leu	Val Asp 360	Met Ala Ala	Gln Val 365	Ala Glu
Gly Met Ala Tyr 370	Met Glu Arg 375	Met Asn	Tyr Ile His 380	Arg Asp	Leu Arg
Ala Ala Asn Ile 385	Leu Val Gly 390	Glu Arg	Leu Ala Cys . 395	Lys Ile	Ala Asp 400
Phe Gly Leu Ala	Arg Leu Ile 405	Lys Asp	Asp Glu Tyr 410	Asn Pro	Cys Gln 415
Gly Ser Lys Phe 420	Pro Ile Lys	Trp Thr 425	Ala Pro Glu	Ala Ala 430	Leu Phe
Gly Arg Phe Thr 435	Ile Lys Ser	Asp Val 440	Trp Ser Phe	Gly Ile 445	Leu Leu
Thr Glu Leu Ile 450	Thr Lys Gly 455	Arg Ile	Pro Tyr Pro 460	Gly Met	Asn Lys
Arg Glu Val Leu 465	Glu Gln Val 470	Glu Gln	Gly Tyr His 475	Met Pro	Cys Pro 480
Pro Gly Cys Pro	Ala Ser Leu 485	Tyr Glu	Ala Met Glu 490	Gln Thr	Trp Arg 495
Leu Asp Pro Glu	Glu Arg Pro	Thr Phe	Glu Tyr Leu	Gln Ser	Phe Leu

505 500 510 Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 520 Thr <210> 42 <211> 525 <212> PRT <213> Homo sapiens <220> <223> Hck kinase (Fig. 18) <220> <221> SITE <222> (289) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (332) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (525) <223> Constant amino acid Y in domain SH1 <400> 42 Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 40 Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 5.5 His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 135

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro

155

150

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Gly	Asn	Met	Leu	Gly 165	Ser	Phe	Met	Ile	Arg 170	Asp	Ser	Glu	Thr	Thr 175	Lys
Gly	Ser	Tyr	Ser 180	Leu	Ser	Val	Arg	Asp 185	Tyr	Asp	Pro	Arg	Gln 190	Gly	Asp
Thr	Val	Lys 195	His	Tyr	Lys	Ile	Arg 200	Thr	Leu	Asp	Asn	Gly 205	Gly	Phe	Tyr
Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
Tyr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Сув	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	Lys	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Lys	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu
Ala 305	Asn	Val	Met	Lys	Thr 310	Leu	Gln	His	Asp	Lys 315	Leu	Val	Lys	Leu	His 320
Ala	Val	Val	Thr	Lys 325	Glu	Pro	Ile	Tyr	Ile 330	Ile	Thr	Glu	Phe	Met 335	Ala
Lys	Gly	Ser	Leu 340	Leu	Asp	Phe	Leu	Lys 345	Ser	Asp	Glu	Gly	Ser 350	Lys	Gln
Pro	Leu	Pro 355	Lys	Leu	Ile	Asp	Phe 360	Ser	Ala	Gln	Ile	Ala 365	Glu	Gly	Met
Ala	Phe 370	Ile	Glu	Gln	Arg	Asn 375	Tyr	Ile	His	Arg	Asp 380	Leu	Arg	Ala	Ala
Asn 385	Ile	Leu	Val	Ser	Ala 390	Ser	Leu	Val	Cys	Lys 395	Ile	Ala	Asp	Phe	Gly 400
Leu	Ala	Arg	Val	Ile 405	Glu	Asp	Asn	Glu	Tyr 410	Thr	Ala	Arg	Glu	Gly 415	Ala
Lys	Phe	Pro	Ile 420	Lys	Trp	Thr	Ala	Pro 425	Glu	Ala	Ile	Asn	Phe 430	Gly	Ser
Phe	Thr	Ile 435	Lys	Ser	Asp	Val	Trp 440	Ser	Phe	Gly	Ile	Leu 445	Leu	Met	Glu
Ile	Val 450	Thr	Tyr	Gly	Arg	Ile 455	Pro	Tyr	Pro	Gly	Met 460	Ser	Asn	Pro	Glu
Val 465	Ile	Arg	Ala	Leu	Glu 470	Arg	Gly	Tyr	Arg	Met 475	Pro	Arg	Pro	Glu	Asn 480
Cys	Pro	Glu	Glu	Leu 485	Tyr	Asn	Ile	Met	Met 490	Arg	Суѕ	Trp	Lys	Asn 495	Arg

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 515 520 525

<210> 43

<211> 512

<212> PRT

<213> Homo sapiens

<220>

<223> Lyn kinase (Fig. 18)

<220>

<221> SITE

<222> (275)

<223> Constant amino acid K in domain SH2

<220>

<221> SITE

<222> (319)

<223> Constant amino acid T in domain SH2

<220>

<221> SITE

<222> (508)

<223> Constant amino acid Y in domain SH1

<400> 43

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
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Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu 115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175

Gly	Asp	Val	Ile 180	Lys	His	Tyr	Lys	Ile 185	Arg	Ser	Leu	Asp	Asn 190	Gly	Gly
Tyr	Tyr	Ile 195	Ser	Pro	Arg	Ile	Thr 200	Phe	Pro	Cys	Ile	Ser 205	Asp	Met	Ile
Lys	His 210	Tyr	Gln	Lys	Gln	Ala 215	Asp	Gly	Leu	Суѕ	Arg 220	Arg	Leu	Glu	Lys
Ala 225	Суз	Ile	Ser	Pro	Lys 230	Pro	Gln	Lys	Pro	Trp 235	Asp	Lys	Asp	Ala	Trp 240
Glu	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly
Gln	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val
Ala	Val	Lys 275	Thr	Leu	Lys	Pro	Gly 280	Thr	Met	Ser	Val	Gln 285	Ala	Phe	Leu
Glu	Glu 290	Ala	Asn	Leu	Met	Lys 295	Thr	Leu	Gln	His	Asp 300	Lys	Leu	Val	Arg
Leu 305	Tyr	Ala	Val	Val	Thr 310	Arg	Glu	Glu	Pro	Ile 315	Tyr	Ile	Ile	Thr	Glu 320
Tyr	Met	Ala	Lys	Gly 325	Ser	Leu	Leu	Asp	Phe 330	Leu	Lys	Ser	Asp	Glu 335	Gly
Gly	Lys	Val	Leu 340	Leu	Pro	Lys	Leu	Ile 345	Asp	Phe	Ser	Ala	Gln 350	Ile	Ala
Glu	Gly	Met 355	Ala	Tyr	Ile	Glu	Arg 360	Lys	Asn	Tyr	Ile	His 365	Arg	Asp	Leu
Arg	Ala 370	Ala	Asn	Val	Leu	Val 375	Ser	Glu	Ser	Leu	Met 380	Cys	Lys	Ile	Ala
Asp 385	Phe	Gly	Leu	Ala	Arg 390	Val	Ile	Glu		Asn 395		Tyr	Thr	Ala	Arg 400
Glu	Gly	Ala	Lys	Phe 405	Pro	Ile	Lys	Trp	Thr 410	Ala	Pro	Glu	Ala	Ile 415	Asn
Phe	Gly	Cys	Phe 420	Thr	Ile	Lys	Ser	Asp 425	Val	Trp	Ser	Phe	Gly 430	Ile	Leu
Leu	Tyr	Glu 435	Ile	Val	Thr	Tyr	Gly 440	Lys	Ile	Pro	Tyr	Pro 445	Gly	Arg	Thr
Asn	Ala 450	Asp	Val	Met	Thr	Ala 455	Leu	Ser	Gln	Gly	Tyr 460	Arg	Met	Pro	Arg
Val 465	Glu	Asn	Cys	Pro	Asp 470	Glu	Leu	Tyr	Asp	Ile 475	Met	Lys	Met	Cys	Trp 480
Lys	Glu	Lys	Ala	Glu 485	Glu	Arg	Pro	Thr	Phe 490	Asp	Tyr	Leu	Gln	Ser 495	Val
Leu	Asp	Asp	Phe 500	Tyr	Thr	Ala	Thr	Glu 505	Gly	Gln	Tyr	Gln	Gln 510	Gln	Pro

<210> 44 <211> 509 <212> PRT <213> Homo sapiens <223> Lck kinase (Fig. 18) <220> <221> SITE <222> (273) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (316) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (505) <223> Constant amino acid Y in domain SH1 Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 90 Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 120 Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 150 155 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 185

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His

		195					200					205					
Tyr	Thr 210	Asn	Ala	Ser	Asp	Gly 215	Leu	Cys	Thr	Arg	Leu 220	Ser	Arg	Pro	Cys		
Gln 225	Thr	Gln	Lys	Pro	Gln 230	Lys	Pro	Trp	Trp	Glu 235	Asp	Glu	Trp	Glu	Val 240		
Pro	Arg	Glu	Thr	Leu 245	Lys	Leu	Val	Glu	Arg 250	Leu	Gly	Ala	Gly	Gln 255	Phe		
Gly	Glu	Val	Trp 260	Met	Gly	Tyr	Tyr	Asn 265	Gly	His	Thr	Lys	Val 270	Ala	Val		
Lys	Ser	Leu 275	Lys	Gln	Gly	Ser	Met 280	Ser	Pro	Asp	Ala	Phe 285	Leu	Ala	Glu		
Ala	Asn 290	Leu	Met	Lys	Gln	Leu 295	Gln	His	Gln	Arg	Leu 300	Val	Arg	Leu	Tyr		
Ala 305	Val	Val	Thr	Gln	Glu 310	Pro	Ile	Tyr	Ile	Ile 315	Thr	Glu	Tyr	Met	Glu 320		
Asn	Gly	Ser	Leu	Val 325	Asp	Phe	Leu	Lys	Thr 330	Pro	Ser	Gly	Ile	Lys 335	Leu		
Thr	Ile	Asn	Lys 340	Leu	Leu	Asp	Met	Ala 345	Ala	Gln	Ile	Ala	Glu 350	Gly	Met		
Ala	Phe	Ile 355	Glu	Glu	Arg	Asn	Tyr 360	Ile	His	Arg	Asp	Leu 365	Arg	Ala	Ala		
Asn	Ile 370	Leu	Val	Ser	Asp	Thr 375	Leu _.	Ser	Cys	Lys	Ile 380	Ala	Asp	Phe	Gly		
Leu 385	Ala	Arg	Leu	Ile	Glu 390	Asp	Asn	Glu	Tyr	Thr 395	Ala	Arg	Glu	Gly	Ala 400		
Lys	Phe	Pro	Ile	Lys 405	Trp	Thr	Ala	Pro	Glu 410	Ala	Ile	Asn	Tyr	Gly 415	Thr		
Phe	Thr	Ile	Lys 420	Ser	Asp	Val	Trp	Ser 425	Phe	Gly	Ile	Leu	Leu 430	Thr	Glu		
Ile	Val	Thr 435	His	Gly	Arg	Ile	Pro 440	Tyr	Pro	Gly	Met	Thr 445	Asn	Pro	Glu		
Val	Ile 450	Gln	Asn	Leu	Glu	Arg 455	Gly	Tyr	Arg	Met	Val 460	Arg	Pro	Asp	Asn		
Cys 465	Pro	Glu	Glu	Leu	Tyr 470	Gln	Leu	Met	Arg	Leu 475	Cys	Trp	Lys	Glu	Arg 480		
Pro	Glu	Asp	Arg	Pro 485	Thr	Phe	Asp	Tyr	Leu 490	Arg	Ser	Val	Leu	Glu 495	Asp		
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Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
                                105
Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
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Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
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Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
145
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Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
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Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys
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Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
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Pro 225	Gln	Asn	Pro	Trp	Ala 230	Gln	Asp	Glu	Trp	Glu 235	Ile	Pro	Arg	Gln	Ser 240
Leu	Arg	Leu	Val	Arg 245	Lys	Leu	Gly	Ser	Gly 250	Gln	Phe	Gly	Glu	Val 255	Trp
Met	Gly	Tyr	Tyr 260	Lys	Asn	Asn	Met	Lys 265	Val	Ala	Ile	Lys	Thr 270	Leu	Lys
Glu	Gly	Thr 275	Met	Ser	Pro	Glu	Ala 280	Phe	Leu	Gly	Glu	Ala 285	Asn	Met	Met
Lys	Ala 290	Leu	Gln	His	Glu	Arg 295	Leu	Val	Arg	Leu	Tyr 300	Ala	Val	Val	Thr
Lys 305	Glu	Pro	Ile	Tyr	Ile 310	Val	Thr	Glu	Tyr	Met 315	Ala	Arg	Gly	Cys	Leu 320
Leu	Asp	Phe	Leu	Lys 325	Thr	Asp	Glu	Gly	Ser 330	Arg	Leu	Ser	Leu	Pro 335	Arg
Leu	Ile	Asp	Met 340	Ser	Ala	Gln	Ile	Ala 345	Glu	Gly	Met	Ala	Tyr 350	Ile	Glu
Arg	Met	Asn 355	Ser	Ile	His	Arg	Asp 360	Leu	Arg	Ala	Ala	Asn 365	Ile	Leu	Val
Ser	Glu 370	Ala	Leu	Cys	Суз	Lys 375	Ile	Ala	Asp	Phe	Gly 380	Leu	Ala	Arg	Ile
Ile 385	Asp	Ser	Glu	Tyr	Thr 390	Ala	Gln	Glu	Gly	Ala 395	Lys	Phe	Pro	Ile	Lys 400
Trp	Thr	Ala	Pro	Glu 405	Ala	Ile	His	Phe	Gly 410	Val	Phe	Thr	Ile	Lys 415	Ala
Asp	Val	Trp	Ser 420	Phe	Gly	Val	Leu	Leu 425	Met	Glu	Val	Val	Thr 430	Tyr	Gly
Arg	Val	Pro 435	Tyr	Pro	Gly	Met	Ser 440	Asn 4	Pro	Glu	Val	Ile 445	Arg	Asn	Leu
Glu	Arg 450	Gly	Tyr	Arg	Met	Pro 455	Arg	Pro	Asp	Thr	Cys 460	Pro	Pro	Glu	Leu
Tyr 465	Arg	Gly	Val	Ile	Ala 470	Glu	Cys	Trp	Arg	Ser 475	Arg	Pro	Glu	Glu	Arg 480
Pro	Thr	Phe	Glu	Phe 485	Leu	Gln	Ser	Val	Leu 490	Glu	Asp	Phe	Tyr	Thr 495	Ala
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